What is claimed is:

1.   A method for determining bcr-abl translocation rearrangements in a biological sample comprising the steps of:

  a)   extracting RNA from a biological sample;

  b)   quantifying the extracted RNA;

  c)   reverse transcribing the RNA to cDNA;

  d)   amplifying the cDNA and detecting a cDNA signal by using the primers and probes set forth in SEQ. ID. NOS. 1-8;

  e)   obtaining a standard curve of cDNA signals from serial dilutions of a leukemic cell line, wherein the cDNA is obtained by repeating steps a) – d) with the RNA from the leukemic cell line and not the sample; and

  f)   extrapolating a measurement of the leukemic cells present in the sample by comparing the signal from step d) with that from step e).

2.   The method of claim 1 wherein the amplification and detection of the cDNA in step d) is accomplished by Real Time PCR.

3.   The method of claim 1 wherein the amplification and detection of the cDNA in step e) is accomplished by Real Time PCR.

4.   The method of claim 1 wherein the measurement in step f) comprises a measurement of the number of leukemic cells present in the sample, wherein a result of less than a certain number of cells is reported as negative, and a result of more than a certain number is reported as positive.

5.   The method of claim 4 wherein wherein a result of less than one leukemic cell per ten thousand total cells is reported as negative, and a result of more than one leukemic cell per ten thousand total cells is reported as positive.

6.   The method of claim 1 wherein the measurement in step f) comprises a

measurement of the total number of leukemic cells present in the sample.

7.   The method of claim 1 further comprising the step of running the cDNA PCR products of step d) on an electrophoretic gel to obtain fragment size and hence identity information.

8.   The method of claim 1 wherein the amplification and detection of the cDNA in step d) is performed in a single container.

9.   The method of claim 1 wherein the amplification and detection of the cDNA in step e) is performed in a single container.

10.   A method of diagnosing CML or ALL by performing the assay of claim 1.

11.   A method of diagnosing CML or ALL by performing the assay of claim 7.

12.   The method of claim 1 wherein the sample includes an RNAse inhibitor.

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